

Title: US-10-825-378-31  
 Perfect score: 1317  
 Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*  
 10: geneseqp2006s:\*

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:27:24 ; Search time 50 Seconds  
 (without alignments)  
 411.394 Million cell updates/sec

Title: US-10-825-378-31  
 Perfect score: 1317  
 Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:\*  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:39:25 ; Search time 177 Seconds  
(without alignments)  
615.003 Million cell updates/sec

Title: US-10-825-378-31  
Perfect score: 1317  
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

GenCore version 5.1.9

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:39:50 ; Search time 22 Seconds  
(without alignments)  
244.032 Million cell updates/sec

Title: US-10-825-378-31  
Perfect score: 1317  
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:22:25 ; Search time 41 Seconds  
(without alignments)  
551.486 Million cell updates/sec

Title: US-10-825-378-31  
Perfect score: 1317  
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

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OM protein - protein search, using sw model

Run on: June 23, 2006, 08:18:55 ; Search time 295 Seconds  
(without alignments)  
736.877 Million cell updates/sec

Title: US-10-825-378-31  
Perfect score: 1317  
Sequence: 1 MRSTPVLRLALLAAALPLGAL.....RTGCRRHDDGGFAVFKAPSA 235

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000